Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-9. (Canceled)

Claim 10. (Currently Amended): A method for identifying a polypeptide that binds with a high affinity to a peptide region in a chosen protein, the peptide region being adjacent to a repulsive peptide region of the chosen protein, the method comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b) contacting the support to which the overlapping peptides are covalently attached with a mixture of polypeptides under conditions enabling binding between the peptides on the support and a polypeptide of the mixture;

(c) washing the support to remove unbound polypeptides of the mixture;

(d) ~~identifying a polypeptide that binds to a first set of contiguous overlapping peptides attached to the support, the first set comprising a first peptide region that binds to the polypeptide with a high affinity; and~~ identifying a first set of contiguous overlapping peptides that bind the polypeptide, the first set comprising a first region that binds to the polypeptide with a high affinity;

(e) ~~identifying a second set of contiguous overlapping peptides attached to the support that binds to the polypeptide, the second set comprising a second peptide region that binds to the polypeptide with a high affinity, the second set~~

~~discontinuous from the first set, and the segment between the first set and the second set comprising the repulsive peptide region of the chosen polypeptide~~, identifying a second set of contiguous overlapping peptides that bind the polypeptide, the second set comprising a second region that binds to the polypeptide with a high affinity, the second set being discontinuous from the first set; and

(f) identifying a segment between the first set and the second set, the segment comprising the repulsive peptide region of the chosen protein, the repulsive peptide region being adjacent to the high affinity peptide regions,

~~wherein~~ the polypeptide that binds to the first peptide region and the second peptide region [[is]] being the polypeptide that binds with a high affinity to the peptide region that is adjacent to the repulsive peptide region of the chosen protein.

Claim 11. (Canceled)

Claim 12. (Previously Presented): The method of claim 10, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 13. (Previously Presented): The method of claim 10, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 14. (Previously Presented): The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 15. (Previously Presented): The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 16. (Previously Presented): The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 17. (Previously Presented): The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 18. (Canceled)

Claim 19. (Previously Presented): The method of claim 10, wherein the mixture of polypeptides comprises a cell lysate.

Claim 20. (Previously Presented): The method of claim 10, wherein the chosen protein is human P-glycoprotein 1.

Claims 21-22. (Canceled)

Claim 23. (Previously Presented): The method of claim 20, wherein the polypeptide is tubulin.

Claim 24. (Previously Presented): The method of claim 10, wherein the chosen protein is human P-glycoprotein 3.

Claim 25. (Canceled)

Claim 26. (Currently Amended): A method for identifying a peptide region in a chosen protein that binds to a polypeptide with a high affinity and is adjacent to a repulsive peptide region of the chosen ~~polypeptide~~ protein, the method comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b) contacting the support to which the overlapping peptides are attached with the polypeptide under conditions enabling binding between the peptide attached to the support and the polypeptide;

(c) washing the support to remove unbound polypeptide;

(d) ~~identifying a first set of contiguous overlapping peptides attached to the support that binds to the polypeptide, the first set comprising the first peptide region that binds to the polypeptide with a high affinity; and~~ identifying a first set of contiguous overlapping peptides that bind the polypeptide, the first set comprising a first region that binds to the polypeptide with a high affinity;

(e) ~~identifying a second set of contiguous overlapping peptides attached to the support that binds to the polypeptide comprising a second peptide region that binds to the polypeptide with a high affinity, the second set discontinuous from the first set, and the segment between the first set and the second set comprising the repulsive peptide region of the chosen polypeptide,~~ identifying a second set of contiguous overlapping peptides that bind the polypeptide, the second set comprising a second region that binds to the polypeptide with a high affinity, the second set being discontinuous from the first set; and

(f) identifying a segment between the first set and the second set, the segment comprising the repulsive peptide region of the chosen protein, the repulsive peptide region being adjacent to the high affinity peptide regions,

thereby identifying the peptide region in the chosen protein that binds to a polypeptide with a high affinity and is adjacent to the repulsive peptide region.

Claims 27-28. (Canceled)

Claim 29. (Previously Presented): The method of claim 26, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 30. (Previously Presented): The method of claim 26, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 31. (Previously Presented): The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 32. (Previously Presented): The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 33. (Previously Presented): The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 34. (Previously Presented): The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 35. (Canceled)

Claim 36. (Previously Presented): The method of claim 26, wherein the chosen protein is human P-glycoprotein 1.

Claims 37-38. (Canceled)

Claim 39. (Previously Presented): The method of claim 36, wherein the polypeptide is tubulin.

Claim 40. (Previously Presented): The method of claim 26, wherein the chosen protein is human P-glycoprotein 3.

Claim 41. (Canceled)

Claim 42. (Withdrawn): A method of identifying a compound that modulates the binding of a polypeptide to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a) providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b) contacting the support to which the overlapping peptides are attached with a candidate compound and the polypeptide under conditions enabling binding between the peptide attached to the support and the polypeptide;

(c) washing the support to remove unbound polypeptides of the mixture; and

(d) detecting binding of the polypeptide to the peptide attached to the support,

wherein a change in the binding of the polypeptide to the peptide attached to the support in the presence of the candidate compound compared to the binding of the polypeptide to the peptide attached to the support in the absence of the candidate compound identifies the candidate compound as a compound that modulates binding of the polypeptide to the peptide in the chosen protein.

Claim 43. (Withdrawn): The method of claim 42, wherein the domain of the chosen protein is a high affinity domain of the chosen protein.

Claim 44. (Withdrawn): The method of claim 42, wherein the polypeptide is known to bind to the chosen protein.

Claim 45. (Withdrawn): The method of claim 42, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 46. (Withdrawn): The method of claim 42, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 47. (Withdrawn): The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 48. (Withdrawn): The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 49. (Withdrawn): The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 50. (Withdrawn): The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 51. (Canceled)

Claim 52. (Withdrawn): The method of claim 42, wherein the chosen protein is human P-glycoprotein 1.

Claims 53-54. (Canceled)

Claim 55. (Withdrawn): The method of claim 52, wherein the polypeptide is tubulin.

Claim 56. (Withdrawn): The method of claim 42, wherein the chosen protein is human P-glycoprotein 3.

Claim 57. (Canceled)

Claim 58. (Withdrawn): A support to which are attached overlapping peptides spanning a complete sequence of at least a domain of a protein.

Claim 59. (Withdrawn): The support of claim 58, wherein the domain of the protein is a high affinity domain of the protein.

Claim 60. (Withdrawn): The support of claim 58, wherein the overlapping peptides span the complete sequence of the entire protein.

Claim 61. (Withdrawn): The support of claim 58, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 62. (Withdrawn): The support of claim 58, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 63. (Withdrawn): The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 64. (Withdrawn): The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 65. (Withdrawn): The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 66. (Withdrawn): The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 67. (Withdrawn): The support of claim 58, wherein the overlapping peptides is covalently attached to the support.

Claim 68. (Withdrawn): The support of claim 58, wherein a polypeptide that binds to a peptide attached to the support is identified as a polypeptide that binds to the protein.

Claim 69. (Withdrawn): The support of claim 58, wherein the chosen protein is human P-glycoprotein 1.

Claims 70-71. (Canceled)

Claim 72. (Withdrawn): The support of claim 58, wherein the chosen protein is human P-glycoprotein 3.

Claims 73-74. (Canceled)

Claim 75. (Previously Presented): The method of claim 26, further comprising identifying the peptide in the chosen protein to which the polypeptide binds the chosen protein.

Claim 76. (Previously Presented): The method of claim 75, wherein the peptide in the chosen protein to which the polypeptide binds is identified by its position on the support.

Claim 77. (Previously Presented): The method of claim 10, wherein identifying the polypeptide that is retained on the support is accomplished by a method selected from the group consisting of performing a Western blot, labeling the polypeptide and identifying the labeled polypeptide, mass spectrometry, 2-D gel electrophoresis, and combinations thereof.

Claim 78. (Canceled)